

OIPE

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/023,894

TIME: 18:47:08

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01142002\J023894.raw

PS

80

ENTERED

3 <110> APPLICANT: CANFIELD, William
 4 KORNFELD, Stuart
 6 <120> TITLE OF INVENTION: EXPRESSION OF LYSOSOMAL HYDROLASE IN CELLS EXPRESSING PRO-N-
 7 ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANIDASE
 9 <130> FILE REFERENCE: 217139US77
 11 <140> CURRENT APPLICATION NUMBER: US/10/023,894
 11 <141> CURRENT FILING DATE: 2001-12-21
 11 <160> NUMBER OF SEQ ID NOS: 22
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 3600
 17 <212> TYPE: DNA
 18 <213> ORGANISM: hybrid
 20 <400> SEQUENCE: 1

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31	cttgggaaaa	acacaacgga	acctactaag	aagagtggag	agcagttaga	gtgtttgcta	360
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81	atacatttta	atctcacgtt	tcaaaataca	aacgatgaag	agttcaaaat	gcagataaca	1860
83	gtggagggtg	acacaaggga	gggacaaaaa	ctgaattcta	cggcccagaa	gggttacgaa	1920
85	aatttagtta	gtcccataac	acttcttcca	gaggcggaag	tcctttttga	ggatattccc	1980

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131 tataggtttg aaatcatggg agaagaagaa atcgctttta aaatgattcg taccaacgtt 3360
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135 aatgacaaca ttgaccacaa tcataaagat gctcagacag tgaaggctgt tctcagggac 3480
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153 Gly Ser Thr Gly Asp Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly
154 20 25 30
157 Lys Leu Ser Arg Asp Gln Tyr His Val Leu Phe Asp Ser Tyr Arg Asp
158 35 40 45
161 Asn Ile Ala Gly Lys Ser Phe Gln Asn Arg Leu Cys Leu Pro Met Pro
162 50 55 60
165 Ile Asp Val Val Tyr Thr Trp Val Asn Gly Thr Asp Leu Glu Leu Leu
166 65 70 75 80
169 Lys Glu Leu Gln Gln Val Arg Glu Gln Met Glu Glu Glu Gln Lys Ala
170 85 90 95
173 Met Arg Glu Ile Leu Gly Lys Asn Thr Thr Glu Pro Thr Lys Lys Ser
174 100 105 110
177 Glu Lys Gln Leu Glu Cys Leu Leu Thr His Cys Ile Lys Val Pro Met
178 115 120 125
181 Leu Val Leu Asp Pro Ala Leu Pro Ala Asn Ile Thr Leu Lys Asp Leu

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186	145					150				155						160
189	Ala	Lys	Pro	Lys	Asn	Pro	Ser	Thr	Asn	Val	Ser	Val	Val	Val	Phe	Asp
190					165					170						175
193	Ser	Thr	Lys	Asp	Val	Glu	Asp	Ala	His	Ser	Gly	Leu	Leu	Lys	Gly	Asn
194				180					185						190	
197	Ser	Arg	Gln	Thr	Val	Trp	Arg	Gly	Tyr	Leu	Thr	Thr	Asp	Lys	Glu	Val
198			195					200					205			
201	Pro	Gly	Leu	Val	Leu	Met	Gln	Asp	Leu	Ala	Phe	Leu	Ser	Gly	Phe	Pro
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205	Pro	Thr	Phe	Lys	Glu	Thr	Asn	Gln	Leu	Lys	Thr	Lys	Leu	Pro	Glu	Asn
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209	Leu	Ser	Ser	Lys	Val	Lys	Leu	Leu	Gln	Leu	Tyr	Ser	Glu	Ala	Ser	Val
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218			275					280					285			
221	Pro	Ala	Tyr	Leu	Leu	Trp	Asp	Leu	Ser	Ala	Ile	Ser	Gln	Ser	Lys	Gln
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225	Asp	Glu	Asp	Ile	Ser	Ala	Ser	Arg	Phe	Glu	Asp	Asn	Glu	Glu	Leu	Arg
226	305					310					315					320
229	Tyr	Ser	Leu	Arg	Ser	Ile	Glu	Arg	His	Ala	Pro	Trp	Val	Arg	Asn	Ile
230				325						330						335
233	Phe	Ile	Val	Thr	Asn	Gly	Gln	Ile	Pro	Ser	Trp	Leu	Asn	Leu	Asp	Asn
234				340					345					350		
237	Pro	Arg	Val	Thr	Ile	Val	Thr	His	Gln	Asp	Val	Phe	Arg	Asn	Leu	Ser
238			355					360				365				
241	His	Leu	Pro	Thr	Phe	Ser	Ser	Pro	Ala	Ile	Glu	Ser	His	Val	His	Arg
242		370					375					380				
245	Ile	Glu	Gly	Leu	Ser	Gln	Lys	Phe	Ile	Tyr	Leu	Asn	Asp	Asp	Val	Met
246	385					390					395					400
249	Phe	Gly	Lys	Asp	Val	Trp	Pro	Asp	Asp	Phe	Tyr	Ser	His	Ser	Lys	Gly
250				405						410						415
253	Gln	Lys	Val	Tyr	Leu	Thr	Trp	Pro	Val	Pro	Asn	Cys	Ala	Glu	Gly	Cys
254				420					425					430		
257	Pro	Gly	Ser	Trp	Ile	Lys	Asp	Gly	Tyr	Cys	Asp	Lys	Ala	Cys	Asn	Asn
258			435					440					445			
261	Ser	Ala	Cys	Asp	Trp	Asp	Gly	Gly	Asp	Cys	Ser	Gly	Asn	Ser	Gly	Gly
262		450					455					460				
265	Ser	Arg	Tyr	Ile	Ala	Gly	Gly	Gly	Gly	Thr	Gly	Ser	Ile	Gly	Val	Gly
266	465					470					475					480
269	Gln	Pro	Trp	Gln	Phe	Gly	Gly	Gly	Ile	Asn	Ser	Val	Ser	Tyr	Cys	Asn
270				485						490						495
273	Gln	Gly	Cys	Ala	Asn	Ser	Trp	Leu	Ala	Asp	Lys	Phe	Cys	Asp	Gln	Ala
274				500					505					510		
277	Cys	Asn	Val	Leu	Ser	Cys	Gly	Phe	Asp	Ala	Gly	Asp	Cys	Gly	Gln	Asp
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285 Tyr Ile Ile Pro Lys Gly Glu Cys Leu Pro Tyr Phe Ser Phe Ala Glu
286 545                      550                      555                      560
289 Val Ala Lys Arg Gly Val Glu Gly Ala Tyr Ser Asp Asn Pro Ile Ile
290                      565                      570                      575
293 Arg His Ala Ser Ile Ala Asn Lys Trp Lys Thr Ile His Leu Ile Met
294                      580                      585                      590
297 His Ser Gly Met Asn Ala Thr Thr Ile His Phe Asn Leu Thr Phe Gln
298                      595                      600                      605
301 Asn Thr Asn Asp Glu Glu Phe Lys Met Gln Ile Thr Val Glu Val Asp
302      610                      615                      620
305 Thr Arg Glu Gly Pro Lys Leu Asn Ser Thr Ala Gln Lys Gly Tyr Glu
306 625                      630                      635                      640
309 Asn Leu Val Ser Pro Ile Thr Leu Leu Pro Glu Ala Glu Ile Leu Phe
310                      645                      650                      655
313 Glu Asp Ile Pro Lys Glu Lys Arg Phe Pro Lys Phe Lys Arg His Asp
314                      660                      665                      670
317 Val Asn Ser Thr Arg Arg Ala Gln Glu Glu Val Lys Ile Pro Leu Val
318                      675                      680                      685
321 Asn Ile Ser Leu Leu Pro Lys Asp Ala Gln Leu Ser Leu Asn Thr Leu
322      690                      695                      700
325 Asp Leu Gln Leu Glu His Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu
326 705                      710                      715                      720
329 Ser Lys Ser Ala Leu Leu Arg Ser Phe Leu Met Asn Ser Gln His Ala
330                      725                      730                      735
333 Lys Ile Lys Asn Gln Ala Ile Ile Thr Asp Glu Thr Asn Asp Ser Leu
334                      740                      745                      750
337 Val Ala Pro Gln Glu Lys Gln Val His Lys Ser Ile Leu Pro Asn Ser
338                      755                      760                      765
341 Leu Gly Val Ser Glu Arg Leu Gln Arg Leu Thr Phe Pro Ala Val Ser
342      770                      775                      780
345 Val Lys Val Asn Gly His Asp Gln Gly Gln Asn Pro Pro Leu Asp Leu
346 785                      790                      795                      800
349 Glu Thr Thr Ala Arg Phe Arg Val Glu Thr His Thr Gln Lys Thr Ile
350                      805                      810                      815
353 Gly Gly Asn Val Thr Lys Glu Lys Pro Pro Ser Leu Ile Val Pro Leu
354                      820                      825                      830
357 Glu Ser Gln Met Thr Lys Glu Lys Lys Ile Thr Gly Lys Glu Lys Glu
358                      835                      840                      845
361 Asn Ser Arg Met Glu Glu Asn Ala Glu Asn His Ile Gly Val Thr Glu
362      850                      855                      860
365 Val Leu Leu Gly Arg Lys Leu Gln His Tyr Thr Asp Ser Tyr Leu Gly
366 865                      870                      875                      880
369 Phe Leu Pro Trp Glu Lys Lys Lys Tyr Phe Leu Asp Leu Leu Asp Glu
370                      885                      890                      895
373 Glu Glu Ser Leu Lys Thr Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn
374                      900                      905                      910
377 Arg Ala Arg Tyr Lys Arg Asp Thr Phe Ala Asp Ser Leu Arg Tyr Val

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382          930          935          940
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386 945          950          955          960
389 Asp Met Phe Pro Glu Glu Phe Asp Lys Thr Ser Phe His Lys Val Arg
390          965          970          975
393 His Ser Glu Asp Met Gln Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met
394          980          985          990
397 Ser Ala Val Gln Pro Leu Asn Ile Ser Gln Val Phe Asp Glu Val Asp
398          995          1000          1005
401 Thr Asp Gln Ser Gly Val Leu Ser Asp Arg Glu Ile Arg Thr Leu
402          1010          1015          1020
405 Ala Thr Arg Ile His Glu Leu Pro Leu Ser Leu Gln Asp Leu Thr
406          1025          1030          1035
409 Gly Leu Glu His Met Leu Ile Asn Cys Ser Lys Met Leu Pro Ala
410          1040          1045          1050
413 Asp Ile Thr Gln Leu Asn Asn Ile Pro Pro Thr Gln Glu Ser Tyr
414          1055          1060          1065
417 Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys Ser Leu Val Thr Asn
418          1070          1075          1080
421 Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala Tyr Lys Asp Lys
422          1085          1090          1095
425 Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu Glu Ile Ala Phe
426          1100          1105          1110
429 Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln Leu Asp
430          1115          1120          1125
433 Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp Asn
434          1130          1135          1140
437 Ile Asp His Asn His Lys Asp Ala Gln Thr Val Lys Ala Val Leu
438          1145          1150          1155
441 Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu
442          1160          1165          1170
445 Leu Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu
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449 Gln Glu Trp Arg Ala Tyr Arg Asp Lys Leu Lys
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469 gagatcaata ccattgtttg ttgattcct atagagacaa tattgctgga aagtcctttc 360
471 agaatcggct ttgtctgccc atgccgattg acgttggtta cacctgggtg aatggcacag 420

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22